

SEQUENCE LISTING

<110> Gao, Zeren
 Hart, Charles E.
 Piddington, Christopher S.
 Sheppard, Paul O.
 Shoemaker, Kimberly E.
 Gilbertson, Debra G.
 West, James W.

<120> GROWTH FACTOR HOMOLOG ZVEGF3

<130> 98-60C1

<160> 50

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1760

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (154)...(1191)

<400> 1

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| attatgtgga aactaccctg cgattctctg ctgccagagc aggctcggcg cttccacccc | 60 |
| agtgacagcct tcccctggcg gtggtgaaag agactcggga gtcgctgctt ccaaagtgcc | 120 |
| cgccgtgagt gagctctcac ccagtcagc caa atg agc ctc ttc ggg ctt ctc | 174 |
| Met Ser Leu Phe Gly Leu Leu | |
| 1 5 | |

| | |
|---|-----|
| ctg ctg aca tct gcc ctg gcc ggc cag aga cag ggg act cag gcg gaa | 222 |
| Leu Leu Thr Ser Ala Leu Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu | |
| 10 15 20 | |

| | |
|---|-----|
| tcc aac ctg agt agt aaa ttc cag ttt tcc agc aac aag gaa cag aac | 270 |
| Ser Asn Leu Ser Ser Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn | |
| 25 30 35 | |

143

09706968.110600

| | |
|---|-----|
| gga gta caa gat cct cag cat gag aga att att act gtg tct act aat Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn 40 45 50 55 | 318 |
| gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr 60 65 70 | 366 |
| gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln 75 80 85 | 414 |
| ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile 90 95 100 | 462 |
| tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile 105 110 115 | 510 |
| tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser 120 125 130 135 | 558 |
| aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro 140 145 150 | 606 |
| tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe 155 160 165 | 654 |
| aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu 170 175 180 | 702 |
| gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu 185 190 195 | 750 |

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144

| | |
|---|----------------------|
| att cga tat ctt gaa cca gag aga tgg cag ttg gac tta gaa gat cta Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu 200 205 210 215 | 798 |
| tat agg cca act tgg caa ctt ctt ggc aag gct ttt gtt ttt gga aga Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg 220 225 230 | 846 |
| aaa tcc aga gtg gtg gat ctg aac ctt cta aca gag gag gta aga tta Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu 235 240 245 | 894 |
| tac agc tgc aca cct cgt aac ttc tca gtg tcc ata agg gaa gaa cta Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu 250 255 260 | 942 |
| aag aga acc gat acc att ttc tgg cca ggt tgt ctc ctg gtt aaa cgc Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg 265 270 275 | 990 |
| tgt ggt ggg aac tgt gcc tgt tgt ctc cac aat tgc aat gaa tgt caa Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln 280 285 290 295 | 1038 |
| tgt gtc cca agc aaa gtt act aaa aaa tac cac gag gtc ctt cag ttg Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu 300 305 310 | 1086 |
| aga cca aag acc ggt gtc agg gga ttg cac aaa tca ctc acc gac gtg Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val 315 320 325 | 1134 |
| gcc ctg gag cac cat gag gag tgt gac tgt gtg tgc aga ggg agc aca Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr 330 335 340 | 1182 |
| gga gga tag ccgcatcacc accagcagct cttgccaga gctgtgcagt Gly Gly * | 1231 |
| 345 | |
| gcagtggtg attctattag agaacgtatg cgttatctcc atccttaatc tcagttgttt gcttcaagga cctttcatct tcaggattta cagtgattc tgaagaggga gacatcaaac agaattagga gttgtgcaac agctcttttg agaggaggcc taaaggacag gagaaaaggt | 1291 1351 1411 |

09706958.110600

145

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| cttcaatcgt | ggaagaaaa | ttaaattgtt | tattaaatag | atcaccagct | agtttcagag | 1471 |
| ttaccatgta | cgtattccac | tagctgggtt | ctgtatttca | gttctttcga | tacggcttag | 1531 |
| ggtaaatgta | gtacagaaaa | aaaactgtgc | aagtgagcac | ctgattccgt | tgccctgctt | 1591 |
| aactctaaag | ctccatgtcc | tgggcctaaa | atcgataaaa | atctggattt | tttttttttt | 1651 |
| tttttgctca | tattcacata | tgtaaaccag | aacattctat | gtactacaaa | cctgtgtttt | 1711 |
| aaaaaggaac | tatgttgcta | tgaattaaac | ttgtgtcgtg | ctgatatga | | 1760 |

<210> 2
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 <213> Homo sapiens

<400> 2

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| Met | Ser | Leu | Phe | Gly | Leu | Leu | Leu | Leu | Thr | Ser | Ala | Leu | Ala | Gly | Gln | 1 | 5 | 10 | 15 |
| Arg | Gln | Gly | Thr | Gln | Ala | Glu | Ser | Asn | Leu | Ser | Ser | Lys | Phe | Gln | Phe | 20 | 25 | 30 | |
| Ser | Ser | Asn | Lys | Glu | Gln | Asn | Gly | Val | Gln | Asp | Pro | Gln | His | Glu | Arg | 35 | 40 | 45 | |
| Ile | Ile | Thr | Val | Ser | Thr | Asn | Gly | Ser | Ile | His | Ser | Pro | Arg | Phe | Pro | 50 | 55 | 60 | |
| His | Thr | Tyr | Pro | Arg | Asn | Thr | Val | Leu | Val | Trp | Arg | Leu | Val | Ala | Val | 65 | 70 | 75 | 80 |
| Glu | Glu | Asn | Val | Trp | Ile | Gln | Leu | Thr | Phe | Asp | Glu | Arg | Phe | Gly | Leu | 85 | 90 | 95 | |
| Glu | Asp | Pro | Glu | Asp | Asp | Ile | Cys | Lys | Tyr | Asp | Phe | Val | Glu | Val | Glu | 100 | 105 | 110 | |
| Glu | Pro | Ser | Asp | Gly | Thr | Ile | Leu | Gly | Arg | Trp | Cys | Gly | Ser | Gly | Thr | 115 | 120 | 125 | |
| Val | Pro | Gly | Lys | Gln | Ile | Ser | Lys | Gly | Asn | Gln | Ile | Arg | Ile | Arg | Phe | 130 | 135 | 140 | |
| Val | Ser | Asp | Glu | Tyr | Phe | Pro | Ser | Glu | Pro | Gly | Phe | Cys | Ile | His | Tyr | 145 | 150 | 155 | 160 |
| Asn | Ile | Val | Met | Pro | Gln | Phe | Thr | Glu | Ala | Val | Ser | Pro | Ser | Val | Leu | 165 | 170 | 175 | |
| Pro | Pro | Ser | Ala | Leu | Pro | Leu | Asp | Leu | Leu | Asn | Asn | Ala | Ile | Thr | Ala | 180 | 185 | 190 | |
| Phe | Ser | Thr | Leu | Glu | Asp | Leu | Ile | Arg | Tyr | Leu | Glu | Pro | Glu | Arg | Trp | 195 | 200 | 205 | |
| Gln | Leu | Asp | Leu | Glu | Asp | Leu | Tyr | Arg | Pro | Thr | Trp | Gln | Leu | Leu | Gly | 210 | 215 | 220 | |
| Lys | Ala | Phe | Val | Phe | Gly | Arg | Lys | Ser | Arg | Val | Val | Asp | Leu | Asn | Leu | 225 | 230 | 235 | 240 |

147

<221> VARIANT
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 <223> Xaa is any amino acid or not present

<221> VARIANT
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 <222> (94)...(113)
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<221> VARIANT
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 <223> Xaa is any amino acid

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| 1 | | | | 5 | | | | | 10 | | | | | | 15 | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | 20 | | | | | 25 | | | | | | | 30 | | |
| Xaa | Xaa | Cys | Xaa | Gly | Xaa | Cys | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | 35 | | | | | 40 | | | | | | 45 | | | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | 50 | | | | 55 | | | | | | 60 | | | | | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Cys | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| 65 | | | | | 70 | | | | 75 | | | | | | | 80 | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | 85 | | | | | | 90 | | | | | | | 95 | |
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | 100 | | | | | 105 | | | | | | | | 110 | |
| Xaa | Cys | Xaa | Cys | | | | | | | | | | | | | | |
| | | | 115 | | | | | | | | | | | | | | |

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 <223> peptide motif

<221> VARIANT

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148

<222> (2)...(2)
 <223> Xaa is Lys or Arg

<221> VARIANT
 <222> (4)...(4)
 <223> Xaa is Asp, Asn or Glu

<221> VARIANT
 <222> (5)...(5)
 <223> Xaa is Trp, Tyr or Phe

<221> VARIANT
 <222> (6)...(16)
 <223> Xaa is any amino acid

<221> VARIANT
 <222> (17)...(20)
 <223> Xaa is any amino acid or not present

<221> VARIANT
 <222> (22)...(22)
 <223> Xaa is Lys or Arg

<221> VARIANT
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 <223> Xaa is Trp, Tyr or Phe

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 Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Gly Xaa Xaa Cys
 20

<210> 5
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 <212> PRT
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<220>
 <223> peptide tag

<400> 5
 Glu Tyr Met Pro Met Glu

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149

1

5

<210> 6
 <211> 1035
 <212> DNA
 <213> Artificial Sequence

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<221> misc_feature
 <222> (1)...(1035)
 <223> n = A,T,C or G

<400> 6

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| atgwsnytnt | tyggnytnyt | nytnytnacn | wsngcnytn | cnngncarmg | ncarggnacn | 60 |
| cargcngarw | snaaytnws | nwsnaartty | carttywsnw | snaayaarga | rcaraayggn | 120 |
| gtncargayc | cncarcayga | rmgnathath | acngtnwsna | cnaayggnws | nathcaywsn | 180 |
| ccnmgnttyc | cncayacnta | yccnmgnaay | acngtnytn | ntggmgnyt | ngtngcngtn | 240 |
| gargaraayg | ntggathca | rytnacntty | gaygarmnt | tyggnytna | rgayccngar | 300 |
| gaygayatht | gyaartayga | ytytgtnar | gtngargarc | cnwsngaygg | nacnathytn | 360 |
| ggnmgntggt | gyggnwsng | nacngtnccn | ggnaarcara | thwsnaargg | naaycarath | 420 |
| mgnathmgnt | tygtnwsnga | ygartaytty | ccnwsngarc | cnngnttytg | yathcaytay | 480 |
| aayathgtna | tgccncartt | yacngargcn | gtwnsnccnw | sngtnytncc | nccnwsngcn | 540 |
| ytncnnytn | ayytnytnaa | yaaygcath | acngcnytn | snacnytna | rgayytnath | 600 |
| mgntayytn | arccngarmg | ntggcarytn | gayytnarg | ayytnaymg | nccnactgg | 660 |
| carynytn | gnaargcntt | ygtnttyggn | mgnaarwsnm | gngtngtna | yytnaaytn | 720 |
| ytncngarg | argtnmgny | ntaywsntgy | acnccnmgna | aytywsntg | nwsnathmgn | 780 |
| gargarytna | armgnacnga | yacnathtty | tgccnggnt | gyytnytn | naarmgntgy | 840 |
| ggnggnaayt | gygcntgyt | yytncaaya | tyaaygart | gycartgyt | nccnwsnaar | 900 |
| gtnacnaara | artaycayga | rgtnytnar | ytngmncna | aracnggnt | nmnggnytn | 960 |
| cayaarwsny | tnacngaygt | ngcnytnar | caycaygarg | artgygaytg | ygntngymgn | 1020 |
| ggnwsnacng | gngng | | | | | 1035 |

<210> 7
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer

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150

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 7
 mgntgyggng gnaaytg 17

<210> 8
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<220>
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<221> misc_feature
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 <223> n = A,T,C or G

<400> 8
 mgntgydsng gnwrytg 17

<210> 9
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 <212> DNA
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<220>
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<400> 9
 carywnccns hrcanck 17

<210> 10
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151

<223> Oligonucleotide primer

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ttytggccng gntggyt

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<211> 17

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<222> (1)...(17)

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<400> 11

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<210> 12

<211> 17

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<210> 13

<211> 17

<212> DNA

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152

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<210> 14

<211> 17

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<213> Artificial Sequence

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<210> 15

<211> 17

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<223> Oligonucleotide primer

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<210> 16

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<213> Artificial Sequence

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153

<223> Oligonucleotide primer

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<223> n = A,T,C or G

<400> 16

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<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

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<222> (1)...(17)

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<400> 17

tgynhnmcm knrmdh

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<210> 18

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer

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<211> 17

<212> DNA

<213> Artificial Sequence

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tgyaartayg aytwygt

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<210> 20

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer

<400> 20

acrwartcrt ayttcca

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<210> 24

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<221> misc_feature

<222> (1)...(17)

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<213> Artificial Sequence

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<223> Oligonucleotide primer

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156

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<211> 21
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<213> Artificial Sequence

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<400> 26
cgtttgatga aagatttggg c 21

<210> 27
<211> 21
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<400> 27
ggaggtctat ataagcagag c 21

<210> 28
<211> 18
<212> DNA
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<400> 28
taacagagga ggtaagat 18

<210> 29
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<400> 29
tcggttctct ttagttct 18

<210> 30
<211> 25
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<210> 31
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<400> 32
gagtggcaac ttccagggcc aggagag 27

<210> 33
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<212> DNA
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158

<223> Oligonucleotide primer

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cttttgctag cctcaaccct gactatc

27

<210> 34

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<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC20.180

<400> 34

cgcgcggttt aaacgccacc atgagcctct tcggg

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<210> 35

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC20.181

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cgatcggcg cgccctatcc tcctgtgctc cc

32

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (226)...(1338)

<400> 36

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120

cagggcgagc gcaggcgagg agagcgcagg gcggcgcggc gtcggtcccc ggagcagaac

180

ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc

237

Met His Arg Leu

| | |
|--|-----|
| atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp 5 10 15 20 | 285 |
| act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala 25 30 35 | 333 |
| aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg 40 45 50 | 381 |
| gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg 55 60 65 | 429 |
| ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His 70 75 80 | 477 |
| tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly 85 90 95 100 | 525 |
| tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val 105 110 115 | 573 |
| gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly 120 125 130 | 621 |
| cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys 135 140 145 | 669 |
| atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys 150 155 160 | 717 |

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| | |
|---|------|
| att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu 165 170 175 180 | 765 |
| acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn 185 190 195 | 813 |
| tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys 200 205 210 | 861 |
| aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn 215 220 225 | 909 |
| cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro 230 235 240 | 957 |
| cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu 245 250 255 260 | 1005 |
| gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn 265 270 275 | 1053 |
| tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe 280 285 290 | 1101 |
| ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys 295 300 305 | 1149 |
| gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val 310 315 320 | 1197 |
| aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg 325 330 335 340 | 1245 |

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161

agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac 1293
 Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His
 345 350 355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa 1338
 His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagttaaagg agggtagagat 1398
 aagagaccct ttctctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458
 agtggttgct gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatatca 1518
 tcaacttcta tacctaagaa tataggattg catttaataa tagtgtttga gggtatatat 1578
 gcacaaacac acacagaaat atattcatgt ctatgtgtat atagatcaaa tgtttttttt 1638
 ttttggata tataaccagg tacaccagag gttacatatg tttgagttag actcttaaaa 1698
 tcctttgcc aataaaggga tggtaaaata tatgaaacat gtccttagaa aatttaggag 1758
 ataaatttat ttttaaatat tgaacacga aacaattttg aatcttgctc tcttaaagaa 1818
 agcatcttgt atattaaaaa tcaaaagatg aggccttctt acatatatcat cttagttgat 1878
 tatt 1882

<210> 37

<211> 370

<212> PRT

<213> Homo sapiens

<400> 37

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
 1 5 10 15
 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
 20 25 30
 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
 35 40 45
 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
 50 55 60
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
 65 70 75 80
 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
 85 90 95
 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
 100 105 110
 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
 115 120 125

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162

Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
 130 135 140
 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
 145 150 155 160
 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
 165 170 175
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
 180 185 190
 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
 195 200 205
 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
 225 230 235 240
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
 275 280 285
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
 325 330 335
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
 340 345 350
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Arg Pro
 355 360 365
 Pro Arg
 370

<210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC21.222

<400> 38

tgagccctcg cccagtcag

163

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<210> 39
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC21.224

<400> 39
 acatacagga aagccttgcc caaaa

25

<210> 40
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC21.223

<400> 40
 aaactaccct gcgattctct gctgc

25

<210> 41
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC21.334

<400> 41
 ggtaaatgga gcttggtga g

21

<210> 42
 <211> 3571
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1049)...(2086)

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164

<400> 42

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| gaattcccg | gtcgaccac | gcgtccggc | gccagggga | aaggaagctg | ggggccgcct | 60 |
| ggcgccattc | ctcgccgag | tgtgggctcc | gtctgccgcg | gggcccgcag | tgccccctgt | 120 |
| ctgcgccagc | acctgttggc | ccgccagctg | gccgccgcg | ccccccgcgc | ccccccgcgc | 180 |
| cgcccgccg | ccagccccc | gccccgcgcg | cgcccgctg | ggggaaagtg | gagacgggga | 240 |
| ggggacaaga | gcgctctctc | agggcagcca | ggccttccct | tagccgcgcc | tgcttagccg | 300 |
| ccacctctcc | tcagccctgc | gtcctgccct | gccttagggc | aggcatccga | gcgctcgcca | 360 |
| ctccgagccg | cccaagctct | cccggcttcc | cgcagcactt | cgccgggtacc | cgagggaact | 420 |
| tcggtggcca | ccgactgcag | caaggaggag | gctccgcggt | ggatccgggc | cagtcccgcg | 480 |
| tcgtccccc | ggcctctctg | cccgcccggg | accgcgcg | cactcgccag | gcacggtccc | 540 |
| ctccccccag | gtgggggtg | ggcgccgcct | gccgcccca | tcagcagctt | tgctattgat | 600 |
| cccaagggtg | tcgctctgct | gccgacctgg | cttccagctt | ggcttggcgg | gaccccgagt | 660 |
| cctcgctgtg | gtcctgtccc | ccaaaactgac | aggtgtctcc | tgcgagtgcg | cacgactcat | 720 |
| cgccgctccc | cgcgctcccc | acccttctt | tctctctctg | ctacccccca | ccccccgcac | 780 |
| ttcgccacag | ctcaggattt | gtttaaacct | tgggaaactg | gttcagggtcc | aggttttgct | 840 |
| ttgatccttt | tcaaaaactg | gagacacaga | agagggtctt | agggaaaact | tttgatggg | 900 |
| attatgtgga | aataccctct | cgattctctg | ctgccagagc | cgccaggcgg | cttccaccgc | 960 |
| agcgcagcct | ttccccgcgt | ggcgtgagcc | ttggagtctg | cgcttcccca | gtgcccgccg | 1020 |
| cgagtgagcc | ctcgccccag | tcagccaa | atg ctc ctc ctc | ggc ctc ctc ctc | | 1072 |

Met Leu Leu Leu Gly Leu Leu Leu
1 5

| | |
|---|------|
| ctg aca tct gcc ctg gcc ggc caa aga acg ggg act cgg gct gag tcc | 1120 |
| Leu Thr Ser Ala Leu Ala Gly Gln Arg Thr Gly Thr Arg Ala Glu Ser | |
| 10. 15 20 | |

| | |
|---|------|
| aac ctg agc agc aag ttg cag ctc tcc agc gac aag gaa cag aac gga | 1168 |
| Asn Leu Ser Ser Lys Leu Gln Leu Ser Ser Asp Lys Glu Gln Asn Gly | |
| 25 30 35 40 | |

| | |
|---|------|
| gtg caa gat ccc cgg cat gag aga gtt gtc act ata tct ggt aat ggg | 1216 |
| Val Gln Asp Pro Arg His Glu Arg Val Val Thr Ile Ser Gly Asn Gly | |
| 45 50 55 | |

| | |
|---|------|
| agc atc cac agc ccg aag ttt cct cat aca tac cca aga aat atg gtg | 1264 |
| Ser Ile His Ser Pro Lys Phe Pro His Thr Tyr Pro Arg Asn Met Val | |
| 60 65 70 | |

| | |
|---|------|
| ctg gtg tgg aga tta gtt gca gta gat gaa aat gtg cgg atc cag ctg | 1312 |
| Leu Val Trp Arg Leu Val Ala Val Asp Glu Asn Val Arg Ile Gln Leu | |
| 75 80 85 | |

| | |
|---|------|
| aca ttt gat gag aga ttt ggg ctg gaa gat cca gaa gac gat ata tgc Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys 90 95 100 | 1360 |
| aag tat gat ttt gta gaa gtt gag gag ccc agt gat gga agt gtt tta Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Ser Val Leu 105 110 115 120 | 1408 |
| gga cgc tgg tgt ggt tct ggg act gtg cca gga aag cag act tct aaa Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Thr Ser Lys 125 130 135 | 1456 |
| gga aat cat atc agg ata aga ttt gta tct gat gag tat ttt cca tct Gly Asn His Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser 140 145 150 | 1504 |
| gaa ccc gga ttc tgc atc cac tac agt att atc atg cca caa gtc aca Glu Pro Gly Phe Cys Ile His Tyr Ser Ile Ile Met Pro Gln Val Thr 155 160 165 | 1552 |
| gaa acc acg agt cct tgc gtg ttg ccc cct tca tct ttg tca ttg gac Glu Thr Thr Ser Pro Ser Val Leu Pro Pro Ser Ser Leu Ser Leu Asp 170 175 180 | 1600 |
| ctg ctc aac aat gct gtg act gcc ttc agt acc ttg gaa gag ctg att Leu Leu Asn Asn Ala Val Thr Ala Phe Ser Thr Leu Glu Glu Leu Ile 185 190 195 200 | 1648 |
| cgg tac cta gag cca gat cga tgg cag gtg gac ttg gac agc ctc tac Arg Tyr Leu Glu Pro Asp Arg Trp Gln Val Asp Leu Asp Ser Leu Tyr 205 210 215 | 1696 |
| aag cca aca tgg cag ctt ttg ggc aag gct ttc ctg tat ggg aaa aaa Lys Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Leu Tyr Gly Lys Lys 220 225 230 | 1744 |
| agc aaa gtg gtg aat ctg aat ctc ctc aag gaa gag gta aaa ctc tac Ser Lys Val Val Asn Leu Asn Leu Leu Lys Glu Glu Val Lys Leu Tyr 235 240 245 | 1792 |
| agc tgc aca ccc cgg aac ttc tca gtg tcc ata cgg gaa gag cta aag Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys 250 255 260 | 1840 |

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166

agg aca gat acc ata ttc tgg cca ggt tgt ctc ctg gtc aag cgc tgt 1888
 Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys
 265 270 275 280

gga gga aat tgt gcc tgt tgt ctc cat aat tgc aat gaa tgt cag tgt 1936
 Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys
 285 290 295

gtc cca cgt aaa gtt aca aaa aag tac cat gag gtc ctt cag ttg aga 1984
 Val Pro Arg Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg
 300 305 310

cca aaa act gga gtc aag gga ttg cat aag tca ctc act gat gtg gct 2032
 Pro Lys Thr Gly Val Lys Gly Leu His Lys Ser Leu Thr Asp Val Ala
 315 320 325

ctg gaa cac cac gag gaa tgt gac tgt gtg tgt aga gga aac gca gga 2080
 Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Asn Ala Gly
 330 335 340

ggg taa ctgcagcctt cgtagcagca cacgtgagca ctggcattct gtgtaccccc 2136
 Gly *
 345

acaagcaacc ttcattccca ccagcgttgg ccgcagggtct ctacgtctgt gatctggct 2196
 atggtaaaga tcttactcgt ctccaaccaa attctcagtt gtttgcctca atagccttcc 2256
 cctgcaggac ttcaagtgtc ttctaaaaga ccagaggcac caagaggagt caatcacaaa 2316
 gcactgcctt ctagaggaag ccagacaat ggtcttctga ccacagaaac aaatgaaatg 2376
 aatgtagatc gctagcaaac tctggagtga cagcatttct ttccactga cagaactggtg 2436
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 aaatgtgccca tgcgtgaaag aaagactgaa gttttcaatg cttggcaact tctccgcaat 2676
 ttggaggaaa ggtgcggtca tggtttgag aaagcacacc tgcacagagg agtggccttc 2736
 ccttcccttc cctctgaggt ggcttctgtg ttctattgtg tatattttta tattctcctt 2796
 ttgacattat aactgttggc ttttctaadc ttgttaaata ttctatttt taccaaaggt 2856
 atttaattatt tttttttatg acaacctaga gcaattattt tttagctgat aatttttttt 2916
 tctaaacaaa attgttatag ccagaagaac aaagatgatt gatataaaaa tcttgttgct 2976
 ctgacaaaaa catatgtatt tcttcttgtt atggtgctag agcttagcgt catctgcatt 3036
 tgaagaatg gatgggggaa gtttttagaa ttggttagtc gcagggacag ttgataaca 3096
 atgtgattat catcaattcc caattctgtt cttagagcta cgaacagaac agagcttgag 3156
 taaatatgga gccattgcta acctaccctt ttctatggga aataggagta tagctcagag 3216

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167

aagcacgtcc ccagaaacct cgaccatttc taggcacagt gttctgggct atgctgcgct 3276
gtatggacat atcctatttta tttcaatact agggttttat tacctttaaa ctcgtctcca 3336
tacacttgta ttaatacatg gatattttta tgtacagaag tatatcattt aaggagtcca 3396
cttattatac tctttggcaa ttgcaaagaa aatcaacata atacattgct tgtaaatgct 3456
taatctgtgc ccaagttttg tggtgactat ttgaattaaa atgtattgaa tcatcaataa 3516
aaataatctg gctatttttg ggaaaaaaa aaaaaaaa aaaaaggcg gccgc 3571

<210> 43

<211> 345

<212> PRT

<213> Mus musculus

<400> 43

Met Leu Leu. Leu Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly Gln
1 5 10 15
Arg Thr Gly Thr Arg Ala Glu Ser Asn Leu Ser Ser Lys Leu Gln Leu
20 25 30
Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg
35 40 45
Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro
50 55 60
His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val
65 70 75 80
Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
85 90 95
Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
100 105 110
Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr
115 120 125
Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe
130 135 140
Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145 150 155 160
Ser Ile Ile Met Pro Gln Val Thr Glu Thr Thr Ser Pro Ser Val Leu
165 170 175
Pro Pro Ser Ser Leu Ser Leu Asp Leu Leu Asn Asn Ala Val Thr Ala
180 185 190
Phe Ser Thr Leu Glu Glu Leu Ile Arg Tyr Leu Glu Pro Asp Arg Trp
195 200 205
Gln Val Asp Leu Asp Ser Leu Tyr Lys Pro Thr Trp Gln Leu Leu Gly
210 215 220
Lys Ala Phe Leu Tyr Gly Lys Lys Ser Lys Val Val Asn Leu Asn Leu
225 230 235 240

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168

<210> 46
<211> 40
<212> DNA
<213> Artificial Sequence

169

<220>

<223> oligonucleotide primer ZC19.372

<400> 46

tgtcgatgaa gccctgaaag acgcgagac taattcgagc

40

<210> 47

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC19.351

<400> 47

acgcgagac taattcgagc tcccaccatc accatcacca cgcgaattcg gtaccgctgg

60

<210> 48

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC19.352

<400> 48

actcactata gggcgaattg cccgggggat ccacgcgaa ccagcggtac cgaattcgcg

60

<210> 49

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC19.371

<400> 49

acggccagtg aattgtaata cgactcacta tagggcgaat tg

42

<210> 50

<211> 1095

<212> DNA

09706968.110600

170

<213> Artificial Sequence

<220>

<223> Fused DNA

<400> 50

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| ctgaaagacg | cgcagactaa | ttcgagetcc | caccatcacc | atcaccacgc | gaattcggta | 60 |
| ccgctgggtc | cgcgtggatc | cggccagaga | caggggactc | aggcggaaac | caacctgagt | 120 |
| agtaaatcc | agttttccag | caacaaggaa | cagaacggag | tacaagatcc | tcagcatgag | 180 |
| agaattatta | ctgtgtctac | taatggaagt | attcacagcc | caaggtttcc | tcatacttat | 240 |
| ccaagaaata | cggctctggt | atggagatta | gtagcagtag | agggaaatgt | atggatacaa | 300 |
| cttacgtttg | atgaaagatt | tgggcttgaa | gacccagaag | atgacatatg | caagtatgat | 360 |
| tttgtagaag | ttgaggaacc | cagtgatgga | actatattag | ggcgcgtggt | tggttctggt | 420 |
| actgtaccag | gaaaacagat | ttctaaagga | aatcaaatta | ggataagatt | tgtatctgat | 480 |
| gaatattttc | cttctgaacc | agggttctgc | atccactaca | acattgtcat | gccacaattc | 540 |
| acagaagctg | tgagtccttc | agtgtaccc | ccttcagctt | tgccactgga | cctgcttaat | 600 |
| aatgctataa | ctgcctttag | taccttgga | gaccttattc | gatattctga | accagagaga | 660 |
| tggcagttgg | acttagaaga | tctatatagg | ccaacttggc | aacttcttgg | caaggctttt | 720 |
| gtttttggaa | gaaatccag | agtgggtgat | ctgaaccttc | taacagagga | ggtaagatta | 780 |
| tacagctgca | cacctcgtaa | cttctcagtg | tccataaggg | aagaactaaa | gagaaccgat | 840 |
| accattttct | ggccaggttg | tctcctgggt | aaacgctgtg | gtgggaactg | tgccctgttgt | 900 |
| ctccacaatt | gcaatgaatg | tcaatgtgtc | ccaagcaaag | ttactaaaaa | ataccacgag | 960 |
| gtccctcagt | tgagacaaa | gaccggtgtc | aggggattgc | acaaatcact | caccgacgtg | 1020 |
| gccctggagc | accatgagga | gtgtgactgt | gtgtgcagag | ggagcacagg | aggatagtgt | 1080 |
| tttggcggat | gagat | | | | | 1095 |

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171